FIG. 2A	
FIG. 2B	

FIG. 2

SEQ ID NO: 5   CCR5
SEQ ID NO: 7   hCC-R2b
SEQ ID NO: 8   hCC-R3
SEQ ID NO: 9   hCC-R1
SEQ ID NO: 10 hCC-R4

I   II

CCR5   1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFFLLT 83
hCC-R2b   6 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVLVLILNCKKLKCLTDIYLLNLAISDLLFLLT 95
hCC-R3   MTTSLDTVETFGTTSYYDDVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNVVVMLILIKYRRLRIMTNIYLLNLAISDLLFLVT 87
hCC-R1   METPNTTEDYDTTEFDYGDATPCQKINERAFGAQLLPPLYSLVFVIGIVGNILVVLVLVQYKRLKNMTSIYLLNLAISDLLFLFT 87
hCC-R4   MNPTDIADTTLDESIYSNYYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLLEVFS 92

III   IV

CCR5   VPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLH 177
hCC-R2b   LPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSV 189
hCC-R3   LPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEFFIILLTIDRYLAIVHAVFALRARTVTFGVIITSIVTWGLAVLAALPEFIFYETEELFEE 182
hCC-R1   LPFWIDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVIITSILALALLASMPGLIFSKTQWEFTH 182
hCC-R4   LPFWGIYALADQWVFGLGLICKMISNMLLVGFYSGIFFLSLARTHVGVIITSLAIWSVAVFASLPGFLFSTCYTERNH 186

FIG. 2A

Replacement Figure.

SEQ ID NO: 11

SEQ ID NO: 12

SEQ ID NO: 13

CCR5   F P Y S Q Y Q F W K N F Q T L K I V I L G L V L P
TTTCCATACAgtcagtatcaattctggaagaattccagacaTTAAAGATAGTCATCTTGGGGCTGGTCCTGCCG

Δccr5 F P Y   I K D S H L G A G P A

deletion

CCR5   L L V M V I C Y S G I L K T L L R C R N E K K R
CTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGG

Δccr5 A A C H G H L L G N P K N S A S V S K •

FIG. 6B

Replacement Figure

FIG. 2

FIG. 2A
FIG. 2B

SEQ ID NO: 5   CCR5
SEQ ID NO: 7   hCC-R2b
SEQ ID NO: 8   hCC-R3
SEQ ID NO: 9   hCC-R1
SEQ ID NO: 10   hCC-R4

FIG. 2A

CCR5 .... 6 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFLLIT ... 83

        1 M|D|YQVSSP|I|YDINYYTSEPCQK|I|NVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFLLIT ... 92

hCC-R2b ... MTTSL|D|TVETFGTTSYYDDVGLL|C|EK|A|DTRALMA|Q|FVPPLYSLVFVFGLLGNMVVVMILIKYRLRL|M|T|N|IYLLNLAISDLLFLIT ... 95

hCC-R3 ...... METPNTIEDYD|I|TTEFD|Y|GDATPCQK|M|NERAFGA|Q|LLPPLYSLVFVIGIVGNILVVLVL|M|QYKRLKNMTSIYLLNLAISDLLFLIT ... 87

hCC-R1 ...... MNPTDIADTTLDESIYSN|Y|LYESIPK|P|CTKEG|I|KAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLLFLIT ... 87

(overline I)   (overline II)

CCR5 .... VPFWAHYA.AA|Q|WD|FGNTMC|Q|LLT|G|LYFIGFFSGIFFIILLTIDRYLA|IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTR|S|QKEG|L|H ... 177

hCC-R2b ...... LP|L|WAH|S|A.ANEWVFGNAMC|K|LFTGLYH|I|G|Y|FGGIFFIILLTIDRYLA|IVHAVFALKARTVTFGVVTSVITWLVAVFASLPGIIFT|K|C|Q|KEDSV ... 189

hCC-R3 ...... LPFW|I|HYVRGHNWVFGHGMC|K|LL|S|G|F|YHTGLYSE|I|FFIILLTIDRYLA|IVHAVFA|I|RARTVTFGVIITSIVTWGLAVL|A|AL|P|EFIFYETEELFEE ... 182

hCC-R1 ...... LPFW|I|D|Y|KLKDDWVFG|D|AMCK|I|L|S|GFYYTGLYSE|I|FFIILLTIDRYLA|IVHAVFALRARTVRFGVIITSIVTWGLAVLAAL|P|EFIFYE|T|EELFEE ... 182

hCC-R4 ...... LPFW|G|IYLA.A|D|QWVFGL|G|LCK|M|ISWMI|V|LVGFYSGIFFVML|M|SI|D|RYLA|IVHAVF|S|LRA|R|T|L|TYG|V|ITSLA|T|WSVAVFASLPGFLFSTCYTE|R|NH ... 186

(overline III)   (overline IV)

Marked-up version

CCR5   F P Y S Q Y Q F W K N F Q T L K I V I L G L V L P
Δccr5 F P Y   deletion   I K D S H L G A G P A

TTTCCATACAgtcagtatcaattctggaagaatttccagacaTTAAAGATAGTCATCTTGGGGCTGGTCCTGCCG

CCR5   L L V M V I C Y S G I L K T L L R C R N E K K R
CTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGG
Δccr5 A A C H G H L L L G N P K N S A S V S K *

FIG. 6B